RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: 10 810,881

Source: TPO

Date Processed by STIC: 9/16/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
    APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
    NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER
VERSION 4.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
<u>Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:</u>

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby,
   Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/810,881

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
   Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino
   Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length
Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing

6 ___ PatentIn 2.0
   "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ___ . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences
   (OLD RULES)
Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES " response to include the skipped sequences

8 ___ Skipped Sequences
   (NEW RULES)
Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's
   (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ___ Invalid <213>
   Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>
Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0
   "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa
"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

```
RAW SEQUENCE LISTING                      DATE: 09/16/2004
PATENT APPLICATION:  US/10/810,881        TIME: 16:05:12

Input Set : A:\CEN5021 NP SEQ LIST 09-10-04.txt
Output Set: N:\CRF4\09162004\J810881.raw
```

```
 3 <110> APPLICANT: Mercken, Marc; Benson, Jacqueline M.
 5 <120> TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES
 7 <130> FILE REFERENCE: CEN5021 NP
 9 <140> CURRENT APPLICATION NUMBER: US 10/810,881
10 <141> CURRENT FILING DATE: 2004-03-26
12 <150> PRIOR APPLICATION NUMBER: US 60/458,474
13 <151> PRIOR FILING DATE: 2003-03-28
15 <150> PRIOR APPLICATION NUMBER: US 60/458,469
16 <151> PRIOR FILING DATE: 2003-03-28
18 <150> PRIOR APPLICATION NUMBER: US 60/458,509
19 <151> PRIOR FILING DATE: 2003-03-28
21 <150> PRIOR APPLICATION NUMBER: US 60/458,510
22 <151> PRIOR FILING DATE: 2003-03-28
24 <160> NUMBER OF SEQ ID NOS: 131
26 <170> SOFTWARE: PatentIn version 3.3
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 125
31 <212> TYPE: PRT
32 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <221> NAME/KEY: MISC_FEATURE
37 <222> LOCATION: (1)..(125)
38 <223> OTHER INFORMATION: Vh1 heavy chain variable region
40 <220> FEATURE:
41 <221> NAME/KEY: MISC_FEATURE
42 <222> LOCATION: (1)..(31)
43 <223> OTHER INFORMATION: framework 1
45 <220> FEATURE:
46 <221> NAME/KEY: MISC_FEATURE
47 <222> LOCATION: (32)..(32)
48 <223> OTHER INFORMATION: complementarity determinng region 1 (CDR1), X is 3-20 (5) of
49         amino acids.
51 <220> FEATURE:
52 <221> NAME/KEY: MISC_FEATURE
53 <222> LOCATION: (33)..(46)
54 <223> OTHER INFORMATION: framework 2
56 <220> FEATURE:
57 <221> NAME/KEY: MISC_FEATURE
58 <222> LOCATION: (47)..(47)
59 <223> OTHER INFORMATION: complementarity determinng region 2 (CDR2), X is 10-30 (17)
60         any amino acids.
62 <220> FEATURE:
```

Handwritten annotations: (p. 7) ; Does Not Comply Corrected Diskette Needed ; Does Not Comply Corrected Diskette Needed (pg. 1-6) ; Pls see item #13 on error summary sheet. "Xaa" can only represent a single amino acid. ; any ; of ; "Xaa" can only represent a single amino acid. 9/16/04

63 <221> NAME/KEY: MISC_FEATURE

RAW SEQUENCE LISTING   DATE: 09/16/2004
PATENT APPLICATION: US/10/810,881   TIME: 16:05:12

Input Set : A:\CEN5021 NP SEQ LIST 09-10-04.txt
Output Set: N:\CRF4\09162004\J810881.raw

```
 64 <222> LOCATION: (48)..(79)
 65 <223> OTHER INFORMATION: framework 3
 67 <220> FEATURE:
 68 <221> NAME/KEY: MISC_FEATURE
 69 <222> LOCATION: (80)..(80)
 70 <223> OTHER INFORMATION: complementarity determinng region 3 (CDR3), X is 25-55 (42)
 71         any amino acids.
 73 <220> FEATURE:
 74 <221> NAME/KEY: MISC_FEATURE
 75 <222> LOCATION: (81)..(125)
 76 <223> OTHER INFORMATION: framework 4
 78 <400> SEQUENCE: 1
 80 Gln Val Gln Leu Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
 81 1               5                   10                  15
 84 Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Xaa
 85                 20                  25                  30
 88 Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Xaa Arg
 89             35                  40                  45
 92 Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu Leu
 93     50                  55                  60
 96 Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa
 97 65                  70                  75                  80
100 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Thr Lys Gly
101                 85                  90                  95
104 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
105             100                 105                 110
108 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
109             115                 120                 125
112 <210> SEQ ID NO: 2
113 <211> LENGTH: 124
114 <212> TYPE: PRT
115 <213> ORGANISM: Homo sapiens
118 <220> FEATURE:
119 <221> NAME/KEY: MISC_FEATURE
120 <222> LOCATION: (1)..(124)
121 <223> OTHER INFORMATION: Vh2 heavy chain variable region
123 <220> FEATURE:
124 <221> NAME/KEY: MISC_FEATURE
125 <222> LOCATION: (1)..(30)
126 <223> OTHER INFORMATION: framework 1
128 <220> FEATURE:
129 <221> NAME/KEY: MISC_FEATURE
130 <222> LOCATION: (31)..(31)
131 <223> OTHER INFORMATION: complementarity determinng region 1 (CDR1), X is 3-20 (7) of
132         any amino acids.
134 <220> FEATURE:
135 <221> NAME/KEY: MISC_FEATURE
136 <222> LOCATION: (32)..(45)
137 <223> OTHER INFORMATION: framework 2
```

W--> (line 84)

Handwritten annotations: "pls see item #13 on error summary sheet." — "of" — ""Xaa" CAN ONLY represent a single amino acid." — "of any" — "Same error"

RAW SEQUENCE LISTING   DATE: 09/16/2004
PATENT APPLICATION: **US/10/810,881**   TIME: 16:05:12

Input Set : **A:\CEN5021 NP SEQ LIST 09-10-04.txt**
Output Set: **N:\CRF4\09162004\J810881.raw**

```
139 <220> FEATURE:                                              Same error
140 <221> NAME/KEY: MISC_FEATURE
141 <222> LOCATION: (46)..(46)
142 <223> OTHER INFORMATION: complementarity determinng region 2 (CDR2), X is 10-30 (16)
    of
143        any amino acids.
145 <220> FEATURE:
146 <221> NAME/KEY: MISC_FEATURE
147 <222> LOCATION: (47)..(78)
148 <223> OTHER INFORMATION: framework 3
150 <220> FEATURE:                                              Same error
151 <221> NAME/KEY: MISC_FEATURE
152 <222> LOCATION: (79)..(79)
153 <223> OTHER INFORMATION: complementarity determinng region 3 (CDR3), X is 15-40 (16)
    of
154        any amino acids.
156 <220> FEATURE:
157 <221> NAME/KEY: MISC_FEATURE
158 <222> LOCATION: (80)..(124)
159 <223> OTHER INFORMATION: framework 4
161 <400> SEQUENCE: 2
163 Gln Ile Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
164 1               5                   10                  15
167 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Xaa Trp
168             20                  25                  30
171 Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala Xaa Arg Leu
172         35                  40                  45
175 Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr Met Thr
176     50                  55                  60
179 Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Xaa Trp
180 65                  70                  75                  80
183 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro Thr Ser Pro
184             85                  90                  95
187 Lys Val Phe Pro Leu Ser Leu Ser Ser Lys Ser Thr Ser Gly Gly Thr
188             100                 105                 110
191 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
192         115                 120
195 <210> SEQ ID NO: 3
196 <211> LENGTH: 100
197 <212> TYPE: PRT
198 <213> ORGANISM: Homo sapiens
201 <220> FEATURE:
202 <221> NAME/KEY: MISC_FEATURE
203 <222> LOCATION: (1)..(100)
204 <223> OTHER INFORMATION: Vh3a heavy chain variable region
206 <220> FEATURE:
207 <221> NAME/KEY: MISC_FEATURE
208 <222> LOCATION: (1)..(31)
209 <223> OTHER INFORMATION: framework 1
211 <220> FEATURE:
212 <221> NAME/KEY: MISC_FEATURE
```

W--> (next to line 167)

```
213 <222> LOCATION: (32)..(32)
214 <223> OTHER INFORMATION: complementarity determinng region 1 (CDR1), X is 3-20 (5) of
any
215       amino acids.
217 <220> FEATURE:
218 <221> NAME/KEY: MISC_FEATURE
219 <222> LOCATION: (33)..(46)
220 <223> OTHER INFORMATION: framework 2
222 <220> FEATURE:
223 <221> NAME/KEY: MISC_FEATURE
224 <222> LOCATION: (47)..(47)
225 <223> OTHER INFORMATION: complementarity determinng region 2 (CDR2), X is 10-30 (18)
of
226       any amino acids.
228 <220> FEATURE:
229 <221> NAME/KEY: MISC_FEATURE
230 <222> LOCATION: (48)..(79)
231 <223> OTHER INFORMATION: framework 3
233 <220> FEATURE:
234 <221> NAME/KEY: MISC_FEATURE
235 <222> LOCATION: (80)..(80)
236 <223> OTHER INFORMATION: complementarity determinng region 3 (CDR3), X is 20-40 (31)
of
237       any amino acids.
239 <220> FEATURE:
240 <221> NAME/KEY: MISC_FEATURE
241 <222> LOCATION: (81)..(100)
242 <223> OTHER INFORMATION: framework 4
244 <400> SEQUENCE: 3
246 Glu Val Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
247 1               5                   10                  15
250 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Xaa
251             20                  25                  30
254 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Xaa Arg
255             35                  40                  45
258 Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
259     50                  55                  60
262 Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa
263 65                  70                  75                  80
266 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Thr Lys Ala
267             85                  90                  95
270 Pro Ser Val Phe
271             100
274 <210> SEQ ID NO: 4
275 <211> LENGTH: 102
276 <212> TYPE: PRT
277 <213> ORGANISM: Homo sapiens
280 <220> FEATURE:
281 <221> NAME/KEY: MISC_FEATURE
282 <222> LOCATION: (1)..(102)
283 <223> OTHER INFORMATION: Vh3b heavy chain variable region
285 <220> FEATURE:
```

(handwritten annotations: "SAme error" appears three times; "W-->" marks line 250; various underlines and circles on lines 214, 225, 236)

```
286 <221> NAME/KEY: MISC_FEATURE
287 <222> LOCATION: (1)..(30)
288 <223> OTHER INFORMATION: framework 1
290 <220> FEATURE:
291 <221> NAME/KEY: MISC FEATURE
292 <222> LOCATION: (31)..(31)
293 <223> OTHER INFORMATION: complementarity determinng region 1 (CDR1), X is 3-20 (5) of
    any
294        amino acids.
296 <220> FEATURE:
297 <221> NAME/KEY: MISC_FEATURE
298 <222> LOCATION: (32)..(45)
299 <223> OTHER INFORMATION: framework 2
301 <220> FEATURE:
302 <221> NAME/KEY: MISC_FEATURE
303 <222> LOCATION: (46)..(46)
304 <223> OTHER INFORMATION: complementarity determinng region 2 (CDR2), X is 5-25 (11)
    of any
305        amino acids.
307 <220> FEATURE:
308 <221> NAME/KEY: MISC_FEATURE
309 <222> LOCATION: (47)..(78)
310 <223> OTHER INFORMATION: framework 3
312 <220> FEATURE:
313 <221> NAME/KEY: MISC_FEATURE
314 <222> LOCATION: (79)..(79)
315 <223> OTHER INFORMATION: complementarity determinng region 3 (CDR3), X is 15-40 (23)
    of
316        any amino acids.
318 <220> FEATURE:
319 <221> NAME/KEY: MISC_FEATURE
320 <222> LOCATION: (80)..(102)
321 <223> OTHER INFORMATION: framework 4
323 <400> SEQUENCE: 4
325 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
326 1               5                   10                  15
329 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Xaa Trp
330             20                  25                  30
333 Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Xaa Arg Phe
334             35                  40                  45
337 Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
338       50                  55                  60
341 Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr Xaa Trp
342 65                  70                  75                  80
345 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
346                 85                  90                  95
349 Ser Val Phe Pro Leu Ala
350             100
353 <210> SEQ ID NO: 5
354 <211> LENGTH: 101
355 <212> TYPE: PRT
356 <213> ORGANISM: Homo sapiens
```

W--> (line 329)

Handwritten annotations: "same error" (three times), "any", "of any", "of"

Handwritten note (circled): The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/16/2004
PATENT APPLICATION: **US/10/810,881**   TIME: 16:05:13

Input Set : **A:\CEN5021 NP SEQ LIST 09-10-04.txt**
Output Set: **N:\CRF4\09162004\J810881.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 32,47,80
Seq#:2; Xaa Pos. 31,46,79
Seq#:3; Xaa Pos. 32,47,80
Seq#:4; Xaa Pos. 31,46,79
Seq#:5; Xaa Pos. 31,46,80
Seq#:6; Xaa Pos. 34,49,82
Seq#:7; Xaa Pos. 32,47,80
Seq#:8; Xaa Pos. 31,46,79
Seq#:9; Xaa Pos. 31,46,79
Seq#:10; Xaa Pos. 25,41,74
Seq#:11; Xaa Pos. 24,40,73
Seq#:12; Xaa Pos. 24,40,73
Seq#:13; Xaa Pos. 24,40,73
Seq#:14; Xaa Pos. 18,34,67
Seq#:15; Xaa Pos. 16,32,65
Seq#:16; Xaa Pos. 23,39,72
Seq#:17; Xaa Pos. 24,40,73
Seq#:18; Xaa Pos. 23,39,72
Seq#:19; Xaa Pos. 23,39,72
Seq#:20; Xaa Pos. 23,40,73
Seq#:21; Xaa Pos. 23,39,72
Seq#:22; Xaa Pos. 23,39,72
Seq#:23; Xaa Pos. 23,39,72
Seq#:24; Xaa Pos. 23,39,72
Seq#:25; Xaa Pos. 23,40,75
Seq#:26; Xaa Pos. 23,39,74
Seq#:27; Xaa Pos. 23,39,72
Seq#:28; Xaa Pos. 23,39,72
Seq#:29; Xaa Pos. 23,39,72
Seq#:30; Xaa Pos. 23,39,72

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104
Seq#:105,106,107,108,109,110,111,112,113,114,115,116,117,118,119,120,121,122
Seq#:123,124,125,126,127,128,129,130,131

VERIFICATION SUMMARY   DATE: 09/16/2004
PATENT APPLICATION: **US/10/810,881**   TIME: 16:05:13

Input Set : **A:\CEN5021 NP SEQ LIST 09-10-04.txt**
Output Set: **N:\CRF4\09162004\J810881.raw**

```
L:84 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16
M:341 Repeated in SeqNo=1
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:16
M:341 Repeated in SeqNo=2
L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:16
M:341 Repeated in SeqNo=3
L:329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:16
M:341 Repeated in SeqNo=4
L:408 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:16
M:341 Repeated in SeqNo=5
L:491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:32
M:341 Repeated in SeqNo=6
L:566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:16
M:341 Repeated in SeqNo=7
L:653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:16
M:341 Repeated in SeqNo=8
L:736 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:16
M:341 Repeated in SeqNo=9
L:811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:16
M:341 Repeated in SeqNo=10
L:886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16
M:341 Repeated in SeqNo=11
L:961 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:16
M:341 Repeated in SeqNo=12
L:1036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:16
M:341 Repeated in SeqNo=13
L:1111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:16
M:341 Repeated in SeqNo=14
L:1178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
M:341 Repeated in SeqNo=15
L:1253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:16
M:341 Repeated in SeqNo=16
L:1332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:16
M:341 Repeated in SeqNo=17
L:1411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:16
M:341 Repeated in SeqNo=18
L:1490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:16
M:341 Repeated in SeqNo=19
L:1569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:16
M:341 Repeated in SeqNo=20
L:1644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:16
M:341 Repeated in SeqNo=21
L:1723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:16
M:341 Repeated in SeqNo=22
L:1802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:16
M:341 Repeated in SeqNo=23
L:1877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:16
M:341 Repeated in SeqNo=24
```

VERIFICATION SUMMARY   DATE: 09/16/2004
PATENT APPLICATION: **US/10/810,881**   TIME: 16:05:13

Input Set : **A:\CEN5021 NP SEQ LIST 09-10-04.txt**
Output Set: **N:\CRF4\09162004\J810881.raw**

L:1952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:16
M:341 Repeated in SeqNo=25